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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/576,693	01/26/2007	Tomoaki Kubo	0230-0238PUS1	1952

2292 7590 03/16/2010

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EXAMINER	
FOX, DAVID T	

ART UNIT	PAPER NUMBER
1638	

NOTIFICATION DATE	DELIVERY MODE
03/16/2010	ELECTRONIC

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

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Office Action Summary	Application No.	Applicant(s)	
	10/576,693	KUBO ET AL.	
	Examiner	Art Unit	
	David T. Fox	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *20 July 2009 & 16 November 2009*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1 and 13-48* is/are pending in the application.

4a) Of the above claim(s) *13-30* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1 and 31-48* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *20 July 2009* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *20 July 2009*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

Applicant's Response

Applicant's claims submitted 16 November 2009 are in compliance with 37 CFR 1.121(c) and 37 CFR 1.75(c). Newly submitted claims 31-48 have been assigned to elected Group I and examined in the instant Office action. Claims 13-30 remain WITHDRAWN as being drawn to a non-elected invention.

The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

Drawings

Applicant's replacement Figures 3 and 7 filed 20 July 2009 have been APPROVED.

Effective Filing Date

The Examiner acknowledges that he previously recited an incorrect filing date for the foreign priority application. However, the Examiner also erred in stating that the effective filing date for this application was the filing date of the foreign priority application. The effective filing date of this application is the filing date of the international application, namely 22 October 2004. The confusion is regretted.

Indefiniteness

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 35, 37, 39, 41, 43, 45 and 47 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 35, line 2, is indefinite in its recitation of "the...phenotypic mutation" which lacks antecedent basis in either claim 1 or claim 31 from which claim 35 depends. Replacement of "mutation" with ---variation--- would obviate this rejection. Dependent claims are included in the rejection.

Anticipation

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 1, 31-36 and 39-40 are rejected under 35 U.S.C. 102(e) as being anticipated by **Wilson et al (US 7,045,679** filed 26 August 1998, submitted by Applicant 20 July 2009).

Claim 1 is drawn to a method of screening genomic DNA fragments comprising cloning unselected plant genomic DNA into a cloning vector to form a genomic library, randomly transforming plants with the genomic DNA fragments, selecting the resultant transgenic plants which exhibit an agriculturally advantageous phenotypic variation, and selecting the genomic DNA fragment which was introduced into the selected plant.

As stated on page 4 of the Office action of 20 February 2009, second full paragraph, the specification does not provide any definition of "selection" as it applies to

genomic fragments. The specification only provides a definition of selecting a population of plants, per paragraph [0038] bridging pages 17 and 18 of the specification.

Claim 31 is drawn to the above method wherein neither the characteristics of the donor plant nor the recipient plant are considered prior to the isolation or introduction of genomic DNA from the donor and into the recipient plants, respectively.

Claims 32-34 are drawn to the method of claims 1 or 31 wherein the genomic fragment is at least 1 kb, is introduced into plant cells or plant tissue via biological or physical methods, and wherein a whole transformed plant is regenerated from the transformed plant cell or plant tissue.

Claims 35-36 are drawn to methods of claims 1 or 31 wherein the agriculturally advantageous phenotypic variation is an increase or decrease in the size or weight of at least a part of the plant or a constituent thereof, or an increase in growth rate or resistance against diseases or pests. As stated in the Office action of 20 February 2009 on page 4, first full paragraph, the agriculturally advantageous phenotypic variation is defined as encompassing an increase or decrease in a specific component or a specific enzyme activity; per page 16 of the specification, the paragraph above paragraph [0035], through paragraph [0036] on page 17.

Claim 35 specifies that said phenotypic variation occurs under normal cultivation conditions, while claim 36 recites that the variation occurs under stress. Claims 39-40 are drawn to the methods of claims 35 and 36, respectively, wherein the transformed plant is of a different species from the plant which was the source of the genomic DNA.

Wilson et al teach a method comprising the isolation of genomic DNA from sorghum and its insertion as fragments into cloning vectors to form a genomic library, wherein the genomic fragments are greater than 20 kb; the random *Agrobacterium*-mediated transformation of corn embryo tissue with said unselected fragments; the regeneration of whole transformed corn plants from said transformed embryo tissue, wherein said transformed plants exhibit improved agronomic characteristics; and the selection of the genomic DNA by Southern blotting. Wilson et al teach that the improved agronomic characteristics include improved yield, stalk strength, root strength, or stay green (which would inherently occur under normal cultivation conditions); as well as improved resistance to the stresses of drought, cold, disease or insects.

See, e.g., column 4, lines 41-61; column 5, lines 33-61; column 6, lines 9-25 and 53-67; column 8, lines 30-50; column 9, lines 27-45; column 10, lines 26-34 and 49-53; column 11, lines 7-37; and claim 1.

One of ordinary skill in the art would also recognize that the introduced genomic DNA would inherently contain coding regions which would express proteins or enzymes, i.e. increased component content or enzyme activity, as contemplated by the instant specification.

Claims 1 and 32-35 are rejected under 35 U.S.C. 102(b) as being anticipated by **Kawasaki et al (US 6,521,408)**.

Kawasaki et al teach a method comprising the isolation of plant genomic DNA fragments of at least 40 kb, inserting said fragments into cloning vectors to produce a genomic library, randomly transforming rice callus cells with said fragments via

Agrobacterium, regenerating whole rice plants and identifying plants which exhibit a restored function, and selecting the introduced genomic fragment by Southern blotting.

See, e.g., column 5, lines 20-30 and 50-55; column 6, lines 12-40; column 7, lines 13-19 and 46-57; column 10, lines 49-59; column 11, lines 46-61; and claim 1. The introduced genomic DNA would inherently comprise genes which would encode proteins or enzymes under normal plant cultivation conditions.

Applicant's arguments filed 20 July 2009 have been fully considered but they are not persuasive. Applicant urges that Kawasaki et al selected recipient plants based on the lack of a particular function, wherein the genomic DNA was utilized to complement said function; so that Kawasaki et al do not teach the random integration of unselected DNA fragments.

The Examiner maintains that the genomic DNA taught by Kawasaki et al was not selected in any way. Random fragments of genomic DNA from the genomic library are contemplated by Kawasaki to be inserted into a recipient plant. Even if it is hoped that some of the genomic fragments possess a desired gene which will complement the function lacking from the original plant to be transformed, none of the genomic fragments were actually selected prior to their introduction. It is well-known in the art that *Agrobacterium*-mediated transformation results in random integration of foreign DNA. It is also noted that the instant specification provides no definition of selection as it applies to isolated genomic DNA, as discussed above. New claim 31 has not been included in this rejection, in view of the prior selection of a particular recipient plant phenotype by Kawasaki et al.

Claims 1, 32-34, 36, 38 and 42 are rejected under 35 U.S.C. 102(b) as being anticipated by **Lazo et al (1991**, Bio/Technology 9:963-967).

Claim 38 is drawn to the method of claim 36 wherein the donor and recipient plant are the same species. Claim 42 is drawn to the method of claim 38 wherein the genomic DNA fragment which was selected from the transformed plant is re-introduced into other plants of the same species.

Lazo et al teach a method of *Arabidopsis* seedling tissue transformation with *Agrobacterium* comprising phage cosmid cloning vectors comprising random 15-20 kb fragments of *Arabidopsis* genomic DNA, wherein regenerated whole *Arabidopsis* plants transformed therewith exhibited the agriculturally advantageous trait of herbicide resistance under herbicide-induced stress conditions, and wherein successive testing of transformed *Arabidopsis* progeny allows the identification of the particular genomic clone conferring the resistance, i.e. the selection of the particular genomic fragment. See, e.g., paragraph bridging pages 965 and 966; page 966, paragraph bridging the columns and Figure 2; paragraph bridging pages 966 and 967.

Applicant's arguments filed 20 July 2009 have been fully considered but they are not persuasive. Applicant urges that Lazo et al preselected the genomic fragment for herbicide resistance, and preselected the recipient plants for herbicide sensitivity, so that they do not teach random transformation with unselected genomic DNA.

The Examiner maintains that Lazo et al created a genomic library of random DNA fragments from an herbicide-tolerant *Arabidopsis* plant. Although the phenotype of the donor plant was known, the isolated genomic DNA fragments were not individually

selected in any way prior to their random introduction into the recipient plants via *Agrobacterium*. Claim 31 is not included in this rejection, since the phenotype of both the donor and recipient plants were considered by Lazo et al.

Claims 1, 32-35 and 39 are rejected under 35 U.S.C. 102(b) as being anticipated by **Olszewski et al (1988**, Nucleic Acids Research 16: 10765-10782).

Olszewski et al teach the biological transformation of tobacco cells with an *Agrobacterium* bacterial strain comprising a plasmid comprising seven random and unselected fragments of approximately 15-20 kb of *Arabidopsis* genomic DNA, wherein the genomic DNA fragments were cloned in the cosmid vector pOCA18, wherein whole tobacco plants were regenerated from the transformed cells, wherein genomic DNA was isolated from the transgenic plants.

See, e.g., page 10768, first, third and fourth full paragraphs; page 10769, second and third paragraphs; page 10770, Figure 1; page 10771, Figure 2 and penultimate paragraph; page 10773, first full paragraph; page 10776, penultimate paragraph; page 10777, Table 3, clones 2-1 through 10-2. The random, unselected genomic DNA fragments would inherently comprise coding sequences which would encode proteins or enzymes under normal cultivation conditions.

Applicant's arguments filed 20 July 2009 have been fully considered but they are not persuasive. Applicant urges that Olszewski et al utilized genomic fragments which were pre-selected for the presence of the AHAS gene conferring herbicide resistance. The Examiner acknowledges this teaching, but notes that Olszewski et al also taught the introduction of random unselected genomic fragments, as discussed above.

Obviousness

Claims 1 and 32-48 are rejected under 35 U.S.C. 103(a) as being unpatentable over **Kawasaki et al (US 6,521,408)** in view of **Hamilton et al (1999**, The Plant Journal 18: 223-229); further in view of **Frary et al (1996**, Plant Cell Reports 16: 235-240), further in view of **Tigchelaar et al (1978**, HortScience 13: 508-513).

Claim 37 is drawn to the method of claim 35 wherein the plant species of the source of genomic DNA and the recipient transformant are the same. Claims 41 and 43 are drawn to the methods of claims 37 and 39, respectively, wherein the selected genomic DNA fragment from the transformed plant is re-introduced into another plant of the same species as the original transformant. Claim 44 is drawn to the method of claim 40 wherein the selected genomic DNA fragment from the transformed plant is re-introduced into another plant of the same species as the original transformant. Claims 45-48 are drawn to the methods of claims 37-40, respectively, wherein the selected genomic DNA fragment from the transformed plant is re-introduced into a plant of a different species from the original transformant.

Kawasaki et al teach a method of biological plant transformation with *Agrobacterium* containing unselected genomic fragments from a plant genomic DNA library, wherein transformed plants exhibiting a trait conferred by a gene in said genomic fragments are identified, as discussed above.

Kawasaki et al also teach the broad applicability of their method to identify and isolate various plant genes present in 10 kb or larger genomic fragments, in particular genes involved in agricultural traits, for the transformation of monocotyledonous or

dicotyledonous plants; wherein the genomic DNA containing the gene conferring said trait may be identified by transformation of plants deficient in that trait (see, e.g., column 2, lines 14-21, 26-28, 43-53, 59-67; column 3, lines 1-10 and 13-15; column 4, lines 43-58; column 5, lines 27-30 and 50-55; column 6, lines 10-40; column 7, lines 12-19 and 43-57; column 11, lines 57-61; column 12, lines 59-67; column 13, lines 1-5).

Kawasaki et al do not explicitly teach the transformation of the same or different plant species as that from which the genomic DNA fragments were originally isolated, the utilization of a genomic DNA fragment which confers a phenotypic variation under stress conditions, or the re-introduction of the selected genomic DNA fragment into other plants of the same or different species.

Hamilton et al teach the production of tomato genomic DNA fragments from cultivated and wild tomato species, at least 100 kb in size, in a library of cloning/plant transformation *Agrobacterium* vectors, for the identification of agricultural genes of interest via tomato transformation therewith via phenotypic complementation, wherein the tomato transformation method of Frary et al was employed. **Hamilton et al suggest** the use of wild tomato genomic DNA fragments which contain a variety of useful agronomic genes. It is well-known in the art that wild relatives comprise genes encoding drought, stress and disease tolerance. See, e.g., page 223, column 2, penultimate paragraph; paragraph bridging pages 223 and 224; page 224; page 227, column 1, second and third paragraphs, column 2, penultimate paragraph.

Frary et al teach the *Agrobacterium*-mediated transformation of tomato tissue explants containing cells, followed by the regeneration of whole transgenic tomato

plants (see, e.g., page 235, column 2; page 236, column 1, top two paragraphs; page 239, Figure 4).

Tigchelaar et al teach tomato mutants with delayed ripening, due to the mutation of ripening genes, wherein ripening involves the degradation of fruit tissue by the enzyme polygalacturonase, and the production of carotenoid compounds and flavor-conferring compounds (see, e.g., paragraph bridging pages 508 and 509; page 511, column 2, Figure 1). Said ripening process of plant part decrease and compound production meets Applicant's definition of an "agriculturally advantageous" trait. Said ripening process occurs under normal plant cultivation conditions.

It would have been obvious to one of ordinary skill in the art to utilize the *Agrobacterium*-mediated method of plant transformation with genomic DNA fragments from a DNA library taught by Kawasaki, and to modify that method by incorporating the tomato genomic DNA library taught by Hamilton et al, the *Agrobacterium*-mediated tomato transformation method taught by Frary et al, and the tomato ripening mutant plants taught by Tigchelaar et al, for the selection of those genomic clones containing ripening genes; given the suggestion by Kawasaki to broadly apply their methods to dicotyledonous plants (which includes tomato), and the suggestion by Hamilton et al to utilize the *Agrobacterium*-mediated transformation of plants with plant genomic fragments for the identification of new agriculturally advantageous genes via phenotypic complementation. The re-introduction of the selected genomic DNA fragments into other tomato plants, to either confirm their function or to confer their advantageous

function to other tomato varieties, would have been obvious to one of ordinary skill in the art.

Regarding claims 36, 40, and dependents, it would have been obvious to utilize the method of tomato transformation with genomic library fragments as taught by Kawasaki et al in view of Hamilton et al, further in view of Frary et al; and to modify that method by incorporating genomic DNA fragments from wild tomato relatives which are known in the art to possess useful genes conferring stress or disease resistance, **as suggested by Hamilton et al**. The re-introduction of the selected genomic DNA fragments into other species, to confirm their function or to confer their advantageous function to other crop plants, would have been obvious as discussed above.

Applicant's arguments filed 20 July 2009 have been fully considered but they are not persuasive. Applicant urges that Kawasaki et al teach the utilization of plants deficient in a particular function as the recipient plants to be transformed, wherein the genomic DNA fragments are hoped to contain a gene to complement that function, as discussed above for the anticipation rejection over Kawasaki et al. The Examiner maintains that these teachings are not excluded by the claims, as discussed above.

Claims 1 and 32-48 are rejected under 35 U.S.C. 103(a) as being unpatentable over **Hamilton (US 5,977,439)** in view of **Hamilton et al (1999**, The Plant Journal 18: 223-229); further in view of **Frary et al (1996**, Plant Cell Reports 16: 235-240), further in view of **Tigchelaar et al** (1978, HortScience 13: 508-513).

Hamilton '439 teaches *Agrobacterium*-mediated tobacco transformation with a cloning vector comprising large fragments of tomato genomic DNA contained in a

genomic library, and suggests *Agrobacterium*-mediated tomato transformation therewith for the identification of agriculturally advantageous genes from said genomic fragments via phenotype complementation, wherein the genomic fragment containing the agriculturally advantageous gene can be identified and isolated, wherein agriculturally advantageous traits including disease resistance are contemplated (see, e.g., column 1, lines 24-27; column 2, lines 51-65; column 3, lines 1-3 and 13-41; column 5, lines 13-25; column 7, lines 35-48; column 8, line 61 through column 9, line 28; column 10, line 61 through column 11, line 34; and claims 1 and 9-11).

Hamilton '439 does not teach tomato transformation or the re-introduction of the selected genomic DNA fragment into other plants of the same or different species.

Hamilton et al (1999) teach *Agrobacterium*-mediated tomato transformation with a vector comprising large genomic DNA fragments from cultivated or wild tomato species, for the identification of agriculturally advantageous genes via phenotype complementation, as discussed above.

Frary et al teach an *Agrobacterium*-mediated method of tomato cell transformation, followed by the regeneration of whole transgenic tomato plants, as discussed above.

Tigchelaar et al teach mutant tomato plants with delayed fruit ripening as discussed above.

It would have been obvious to one of ordinary skill in the art to utilize the *Agrobacterium*-mediated method of plant transformation with tomato genomic DNA fragments from a DNA library taught by Hamilton, and to modify that method by

incorporating the wild or cultivated tomato genomic DNA library taught by Hamilton et al, the *Agrobacterium*-mediated tomato transformation method taught by Frary et al, and the tomato ripening mutant plants taught by Tigchelaar et al, for the selection of those genomic clones containing ripening genes or disease resistance genes; given the suggestion by Hamilton to broadly apply her methods to dicotyledonous plants including tomato, and the suggestion by Hamilton et al to utilize the *Agrobacterium*-mediated transformation of plants with plant genomic fragments for the identification of new genes via phenotypic complementation. The re-introduction of the selected genomic DNA fragment into other plants of the same or different species would have been obvious as discussed above.

Applicant's arguments filed 20 July 2009 have been fully considered but they are not persuasive. Applicant urges that Hamilton '439 uses the genomic library for the identification of complementing genes, and so does not teach unselected genomic DNA. Applicant further urges that Hamilton et al (1999) utilizes kanamycin-mediated selection of the genomic library in Figure 2.

The Examiner maintains that the genomic library of Hamilton '439 is not preselected, even if it is hoped that said library contains a particular gene of interest. The Examiner further notes that Hamilton et al (1999) utilized a bacterial kanamycin resistance gene located on the plasmid vector, outside of the cloning site for the plant genomic DNA, merely to identify transformed bacteria which contain the plasmid vector, prior to plant transformation therewith. The pre-selection of individual genomic DNA fragments was not taught.

Claims 1, 32-38 and 41-42 are rejected under 35 U.S.C. 103(a) as being unpatentable over **Lazo et al (1991**, Bio/Technology 9:963-967) in view of **Valvekens et al (1988**, Proc. Natl. Acad. Sci. USA 85: 5536-5540), further in view of **Haughn et al (1986**, Molecular and General Genetics 204: 430-434).

Lazo et al teach *Agrobacterium*-mediated transformation of herbicide-sensitive *Arabidopsis* seedling tissue with genomic libraries comprising random 15-20 kb genomic DNA fragments, some of which may comprise a putative herbicide-resistance gene from the herbicide-resistant GH50 *Arabidopsis* strain; for the identification of the particular genomic fragment containing the herbicide resistance gene via phenotypic complementation in regenerated transformed plants; followed by the selection of the genomic fragment for the further isolation of the gene; followed by the re-introduction of the selected genomic fragment into other *Arabidopsis* plants to confirm its function. **Lazo et al suggest** the broad applicability of their method to identify any *Arabidopsis* gene which confers a screenable or selectable phenotype.

See, e.g., page 963, column 1, bottom paragraph; paragraph bridging pages 965 and 966; page 966, paragraph bridging columns 1 and 2; and paragraph bridging pages 966 and 967.

Lazo et al do not teach the transformation of individual *Arabidopsis* cells followed by the regeneration of whole transgenic *Arabidopsis* plants therefrom, or the use of other *Arabidopsis* genes conferring desirable traits under normal cultivation conditions.

Valvekens et al teach an *Agrobacterium*-mediated method of *Arabidopsis* root tissue comprising cells, followed by the regeneration of whole transformed *Arabidopsis* plants from the transformed cells. See, e.g.,paragraph bridging pages 5536 and 5537; page 5537, Figure 2.

Haughn et al teach the herbicide-resistant *Arabidopsis* strain GH50 (see, e.g., page 430, column 2, second and third full paragraphs; page 431, column 2, second and third full paragraphs).

It would have been obvious to one of ordinary skill in the art to utilize the *Agrobacterium*-mediated transformation of herbicide-sensitive *Arabidopsis* plants with genomic DNA fragments as taught by Lazo et al, and to modify that method by incorporating the particular transformation method of Valvekens et al and the genomic fragments from the herbicide-resistant *Arabidopsis* strain GH50, to identify and select the herbicide resistance gene from the genomic clones containing it, as suggested by Lazo et al. Choice of known method of *Arabidopsis* transformation would have been the optimization of process parameters. The herbicide resistance gene confers increased plant growth and resistance to environmental (chemical) stress, thus meeting Applicant's definition of an agriculturally advantageous gene. Moreover, it would have been obvious to utilize the above method to identify any agronomic gene from *Arabidopsis*, as suggested by Lazo et al.

Applicant's arguments filed 20 July 2009 have been fully considered but they are not persuasive. Applicant urges that Lazo et al utilize a pre-selected genomic DNA fragment, since said fragment is isolated from an herbicide-resistant plant, and since

they hope that said fragment will complement herbicide sensitivity. The Examiner maintains that individual genomic fragments from the source plant were not preselected, as discussed above. Claim 31 has not been included in this rejection.

Conclusion

Claims which are drawn to the method of claim 1 wherein neither the source plant nor the recipient transformant plant has been pre-selected for a particular phenotype (claim 31); *and* wherein either 1) the source plant and the recipient plant are of the same species, *or* 2) wherein the selected genomic fragment is isolated from the transformed plant and re-introduced into another plant of any species; would be deemed free of the prior art; given the failure of the prior art to teach or reasonably suggest this combination of steps.

The only prior art which teaches the elements of claim 31, namely Wilson et al, is drawn to the use of genomic DNA from one plant species to confer an advantageous phenotype to a different species via heterosis, wherein the genomic DNA does not need to be isolated, and wherein the transformed plant exhibiting the desired phenotype is instead crossed to other plants to confer the same phenotype. Thus, Wilson et al teach away from the subject matter set forth above.

No claim is allowed.

Contact Information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to David T. Fox whose telephone number is (571) 272-0795. The examiner can normally be reached on Monday through Friday from 10:30AM to 7:00PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg, can be reached on 571-272-0975. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

/David T Fox/

Primary Examiner, Art Unit 1638

March 11, 2010